Copyright

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Listing first 45 summaries
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1: geneseqp1990s:*
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geneseqp1980s:*
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SUMMARIES

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ALIGNMENTS

RESULT 1 ABP51670

ABP51670 standard; peptide; 15 8

ABP51670;

01-OCT-2002 (first entry)

Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:2.

TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

Homo sapiens.

Synthetic.

WO200246238-A2

13-JUN-2002.

05-DEC-2001; 2001WO-US047656

05-DEC-2000; 2000US-0251448P 04-MAY-2001; 2001US-0288889P 29-MAY-2001; 2001US-0294068P

(ALEX-) ALEXION PHARM INC.

Bowdish 3 Barbas-Frederickson ß Renshaw M;

WPI; 2002-566610/60.

A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoletin or thrombopoetin mimetic.

Claim 19; Page 6; 113pp; English.

The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline and rearboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as stimulator of proliferation, differentiation and maturation of

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RESULT 2
ADQ16585
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Best Local s
Matches 15
                 The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunostherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
                                                                                                                                                                                                                         New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic therapeutics, in cell isolation strategies, and for diagnostics or their progenitors. (I) is useful for diagnostics or suffering from deficiency in cell populations caused by disease, algorates or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73373 and ABPS1695 to ABPS1696 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoletin; EPO; thrombopoletin; TPO; immunosuppressive;
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represents a TPO mimetic peptide.

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The present invention describes an immunoglobin molecule or its fragment CC (ast a portion of the complementary determining region (CDR) are corresponding to at the complementary determining region (CDR) are cc replaced or fused with biologically active peptides e.g. a peptide cc mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has cc a stimulator of proliferation, differentiation and maturation of a stimulator of proliferation, differentiation and maturation of cc haematopoietic cells, and a stimulator of haematopoietic, so the consequence or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, is useful for increasing the cc production or tred blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell populations caused by disease, cc disorders or treatments related to the suppression of haematopoiesis.
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ABP51687
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04-MAY-2001;
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        cc least a portion of the complementary determining region (CDN) are replaced or fused with biologically active peptides e.g. a peptide commetic such as an erythropoietin (EDN) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has the stimulator of proliferation, differentiation and maturation of antimulator of proliferation, differentiation and maturation of the haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of proliferation, differentiation or growth of the promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or correct of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or their progenitors. (I) is useful for diagnostics or therapeutics, in the cell isolation strategies, and for treating patients
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
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         CC (I) comprising a region where amino acid residues corresponding to at CC (east a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide CC mimetic such as an erythropoeietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as CC astimulator of proliferation, differentiation and meturation of CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, where (I) is contacted with corresponding to a portion of CDR is replaced with a region where amino acid residues corresponding to production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or corresponding the production of red blood cells, where (I) is contacted with haematopoietic production of red blood cells, where (I) is contacted with haematopoietic
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29-MAY-2001; 2001US-0294068P
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or their progenitors
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at CC least a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide (CDR) mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, CC that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of CC a stimulator of proliferation, differentiation or growth of the cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and can be useful corresponding to promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or corresponding to more of its CDRs fused to an EPO mimetic, is useful for increasing the
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(I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (EPO) or thrombopoletin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful for stimulator of promegakaryocytes or megakaryocytes, where (I) is contacted with production. (I) with a region where amino acid residues corresponding to
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least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic completed of proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                       The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are
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Synthetic.
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DB; ABQ73362.
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Pred. No. :
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                                                                                                                                                      A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoletin or thrombopoetin mimetic.
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29-MAY-2001; 2001US-0294068P.
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haematopoietic cell; haematopoiesis.
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietic cells.

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antianaemic;
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The present invention describes an immunoglobin molecule or its fra (1) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EBPO) or thrombopoietin (TPO) mimethat is flanked with proline at its carboxy terminus. (1) has antianaemic, haemostatic and nephrotropic activities, and can be us

and can be used

mimetic,

The present invention describes an immunoglobin molecule or its free (I) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (BPO) or thrombopoletin (TPO) min that is flanked with proline at its carboxy terminus. (I) has

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Example

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5; 113pp; English

thrombopoetin mimetic.

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CC a stimulator of proliferation, differentiation and maturation of CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful CC form stimulating proliferation, differentiation or growth of CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet CC production. (I) with a region where amino acid residues corresponding to CC a portion of CDR is replaced with an EPO mimetic, or which has one or CC more of its CDRs fused to an EPO mimetic, is useful for increasing the CC production of red blood cells, where (I) is useful for increasing the CC stem cells or their progenitors. (I) is useful for diagnostics or CC therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, CC disorders or treatments related to the suppression of haematopoiesis. CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
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Best Local S
Matches 15
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04-MAY-2001;
29-MAY-2001;
                                                                                                                                           A novel immunogen molecule comprising a region in which amino actoresidues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin o
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Synthetic.
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The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an exythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in treating thrombocytopenia as a result of chemotherapy, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wior a TPO mimetic, useful for treating thrombocytopenia.
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Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                            New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                              Sequence 18
                                                                                                                                                                                                                                                                                                                                                                    Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ16619 standard; peptide;
                                                                                                     The present residues.
                                                                                                                                                                                                                                                       Example 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO mimetic peptide with random flanking residues
                                                                                                                                                                                                                                                                                                                                                                                             (ALEX-)
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DB; ADQ16620.
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                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                             ALEXION
     IEGPTLRQWLAARAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEGPTLROWLAARAP
                                                                                                                                                                                                                                                     SEQ ID NO 39; 107pp; English.
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K
                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or chronic diseases such as idiopathic thrombocytopenia. ence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                           100.0%; Score 80; DI
100.0%; Pred. No. 2.1
tive 0; Mismatches
                                                                                                               represents a TPO mimetic
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                                         2.1e-06;
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                                                    DB 8;
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                                                                                                                 peptide with flanking
                                                  Length 18;
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                            Indels
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                            Gaps
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ADQ16646
ID ADQ16
XX ADQ16
XX ADQ16
XX D9-SE
DT 09-SE
XX TPO m
XX Immun
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ADQ16621
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                                                                                                                                                                                                                                                               Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
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immunotherapy; t
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                            TPO mimetic peptide SEQ ID NO:65.
                                                          09-SEP-2004
                                                                                                                  ADQ16646 standard; peptide; 18
                                                                                                                                                                                                                                                                                                        Sequence 18
                                                                                                                                                                                                                                                                                                                                      The present residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 41; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2002; 2002US-00307724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ16621;
immunoglobulin; complementarity determining region; CDR; peptide mimetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                     IEGPTLROWLAARAP 15
                                                                                                                                                                                         IEGPTLROWLAARAP 17
                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide with random flanking residues SEQ ID NO:41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frederickson S,
                                                         (first entry)
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                                                                                                                                                                                                                                                               100.0%;
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Pred. No. 2.1e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renshaw M;
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Search completed: December 20, Job time : 155 secs

2004,

13:51:00

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                           S
                                                          Query Match
Best Local S
Matches 15
                                                                                                                                                   The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunoguppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                            New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced without a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-460973/43.
N-PSDB; ADQ16645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 66; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-) ALEXION PHARM INC.
w
                     1 IEGPTLROWLAARAP
                                                              15;
                                                                            Similarity
IEGPTLROWLAARAP
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frederickson S,
                                                                            100.0%;
 17
                                                              0
                                                                            Score 80; DB 8;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renshaw M;
                                                              Mismatches
                                                                                         Length 18
                                                               Indels
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Scoring table: Sequence:

Perfect score:

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Sequence Sequence Sequence

Sequence

sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence

17, Appl
185, App
118, Appl
118, Appl
1194, App
232, App
1194, Appl
1295, Appl
1296, Appl
1297, Appl
1207, Appl
1207, Appl
1207, Appl
1207, Appl
1207, App

Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodatta/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodatta/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodatta/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodatta/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodatta/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodatta/1/iaa/backfIles1.pep:*
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. (without alignments)
26.886 Million cell updates/sec
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80
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       GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                        US-08-764-640-133
US-08-973-225-13
US-08-973-225-13
US-09-244-298A-13
US-09-244-298A-13
US-09-516-704-193
US-09-516-704-193
US-09-519-090-13
US-09-519-090-13
US-09-619-090-13
US-09-619-090-13
US-09-619-082B-26
US-09-619-082B-26
US-09-619-082B-26
US-09-619-082B-32
US-09-619-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 185, Appl Sequence 17, Appl Sequence 17, Appl Sequence 185, Appl Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION UNMBER: 36,392
REFERENCE/DOCKET NUMBER: 978.281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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US-08-764-640-13
    ; MOLECULE TYPE:
US-08-764-640-13
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APPLICANT:
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ADDRESSEE: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                 LENGTH: 14 amino a
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K
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Cwirla, Steven E.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Poddururi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08764640
                                                                                                                        14 amino acids
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                           peptide
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US-09-832-230A-185
US-08-764-640-194
US-08-764-640-232
US-08-764-640-232
US-08-973-225-194
US-08-973-225-220
US-08-973-225-220
US-09-244-298A-194
US-09-244-298A-232
US-09-244-298A-232
US-09-244-298A-232
US-09-516-704-194
US-09-516-704-232
US-09-516-704-232
US-09-549-090-18
US-09-549-090-18
US-09-549-090-18
US-09-549-090-18
US-09-549-090-18
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Result No.

Score

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RESULT 3
US-08-973-225-13
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Patent No. 5869451 5837683
GENERAL INFORMATION:
APPLICANT: Dower, Willia
APPLICANT: Garrett, Rona
APPLICANT: Cwirla, Steve
APPLICANT: Gates, Christ
APPLICANT: Schatz, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-764-640-193
Sequence 13, Application US/08973225A
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                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                MOLECULE TYPE: peptide -08-764-640-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
                                                                                                                                                                                                                                                                                                    TELEPHONE: 919-248-10 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY APPLICATION: 514
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                                                                                                                                                                                     TYPE: STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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INFORMATION:
INFORMATION:
CANT: Dower, William J.
CANT: Ronald W.
                                                                                            1 IEGPTLRQWLAARA 14
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                                                                      IEGPTLROWLAARA 14
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                                                                                                                                    Conservative
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Cwirla, Steven E.
Gates, Christian
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100.0%; Pr
                                                                                                                                             91.2%; Score 73; DB 2;
100.0%; Pred. No. 2e-05;
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                                                                                                                                    Mismatches
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2e-05;
hes 0; Indels
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                                                                                                                             0,
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; Patent No. 6083913
; GENERAL INFORMATION: Dower, William J.
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
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                                                                                                                                                                                                                                        Sequence 193, Applicat:
Patent No. 6083913
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
         Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/973,225A
APPLICATION NUMBER: US/08/973,225A
ETIING DATE: 04-Dec-1997
ATTORNEY/BAGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                      APPLICANT: Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HILDIEC, ROBERT T.
REGISTRATION NUMBER: 36,992
REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
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Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
Wrighton, PEPTIDES AND COMPOUNDS THAT BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CTTY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                           Application US/08973225A
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                   Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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/ 100.0%; Pr
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-08-973-225-193
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Best Local Similarity
Matches 14; Conserv
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CLARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13,
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                                                                                                                                                                                                                          APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                    ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
APPLICATION NUMBER:
                                                                                                                                  COUNTRY: U
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NUMBER: US/08/973,225A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
                                                                                                                                                      USA
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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100.0%; Pred. No. 2e-05;
Live 0; Mismatches
US/09/244,298A
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Patent No. 61
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                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                       REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                  STATE: NC
                                                                                                                                                                                                                                                      SOFTWARE:
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TOPOLOGY: 1i
                                                                                           TELEPHONE:
                                              ENGTH:
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                            amino acid
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                                              14 amino acids
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Podduturi, Surekha
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Hendren, Richard W.
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linear
                                                                                           919-248-1000
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                                                                                                                                                                                                                     US/09/244,298A
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                                                                              193:
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US-09-516-704-193
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                RESULT 8
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/ BEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-516-704-13
                                                                                                                    Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                     NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
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GENERAL INFORMATION:
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: -UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Unition Deheater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dower, William J
                                                                                                                      14;
                                                                                   1 IEGPTLROWLAARA 14
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                                                                                                                                      Similarity
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Similarity 100.0%; F
                                                       IEGPTLROWLAARA 14
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                                                                                                                      Conservative
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                               91.2%; Score 73; DB
100.0%; Pred. No. 2e-
tive 0; Mismatches
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; Pred. No. 2e-
0; Mismatches
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. 2e-05;
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5. 2e-05;
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                                                                                                                                              Length 14;
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RESULT 9
US-09-549-090-13
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                                                                                                                                                                                                  Patent No. 6465430
GENERAL INFORMATION:
APPLICANT: Dowe
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Best Local Similarity
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Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION NUMBER: US/09/516,704

FILING DATE: 01-Mar-2000

CLASSIFICATION: <URKnown>
ATTORNEY/AGBNT INFORMATION:

NAME: HTUBLEC, Robert T.

REGISTRATION NUMBER: 36,392
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaco Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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TYPE: amino acid
                                                                                                                                                                                                                                                          Application US/09549090
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                                                        Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                  Dower, William J
                                                                                                                                                          Barrett, Ronald W.
Cwirla, Steven E.
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Hendren, Richard W.
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Balasubramanian, Palaniappan
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Cwirla, Steven E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 193, Application US/09549090 Patent No. 6465430 GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK:
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILLING DATE: 13-APT-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                    Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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Barrett, Ronald W.
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                                                                                               ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/973,225 FILING DATE: <Unknown>
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ZIP: 27709
                                                            COUNTRY: USA
ZIP: 27709
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                                                                                                                                                                                                                                                                                                     Duffin, David J. Gates, Christian Haselden, Sherril S. Mattheakis, Larry C.
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                                                                                                                                                                                                                                                                                             Schatz, Peter J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.2%; Score 73; DB
100.0%; Pred. No. 2e-
tive 0; Mismatches
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2e-05;
hes 0; Indels
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US-09-832-230A-13
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Matches
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; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-832-230A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Itent No. 6506362
GENERAL INFORMATION:
GENERAL INFORMATION: William J. et al
APPLICANT: DOWER, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   ZIP: 27709

ZIP: 27709

ZIP: 27709

ZIP: 27709

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/832,230A

PPLICATION NUMBER: US/09/832,230A

PILING DATE: 10-Apr-2001

CLASSIFICATION: <UNKNEWN-

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/973,225
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: HTUBLEC, Robert T.
REGISTRATION UNMER: 95,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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SEQUENCE DESCRIPTION: SEQ ID NO: 193:
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                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                       TELEPHONE: 919-248-1000
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                                                                                                                                              LENGTH: 14 amino acids
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100.0%; Pr
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Pred. No. 2e-05;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-09-832-230A-193
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US-09-832-230A-193
i Sequence 193, Application US/09832230A
i Patent No. 6506362
i Patent No. HORMATION:
                                                                                                                                                                                                         US-09-428-082B-13
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                                           Sequence 13, Application US/09428082B
PATENT NO. 6660843
GENERRAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHUAN-FA
APPLICANT: CHUAN-FA
APPLICANT: GOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           Matches
CURRENT APPLICATION NUMBER: US/09/428,082B CURRENT FILING DATE: 1999-10-22
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Best Local Similarity
                                     FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,230A
FILLING DATE: 10-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT.INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dower, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                              1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hrubiec,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                  91.2%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 2e-05;
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RESULT 15
US-09-428-082B-29
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Matches 14
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                                                                                                                                                                  Sequence 29, Application US/09428082B Patent No. 6660843 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHESTHAM, JANST C.
APPLICANT: BOOME, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED BEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,0828
CURRENT FILING DATE: 1999-10-22
CURRENT FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6660843
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FEIGE, ULRICH APPLICANT: LIU, CHUAN-FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/428,0828
CURRENT FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (14)...(14)
OTHER INFORMATION: At position 14, amino acid linker to an identical sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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100.0%; Pred. No.
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PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PatentIn version 3.1

SEQ ID NO 29

LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: TPO-MIMETIC PEPTIDE
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15) \( \text{.}(16) \)
OTHER INFORMATION: Position 16 bromoscetyl group linked to sidechain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14) \( \text{.}(14) \)
OTHER INFORMATION: At position 14, amino acid linker attached N-to-C to Lys and to a
COTHER INFORMATION: nother linker and an identical sequence
US-09-428-0828-29
Search completed: December 20, 2004, 13:55:42 Job time : 38 secs
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1 IEGPTLRQWLAARA 14
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                              Score
            88888888888888
        Match
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                              Length
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gnz_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
gnz_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
gnz_6/ptodata/1/pubpaa/US09_RUBCOMB.pep:*
gnz_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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gnz_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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gnz_6/ptodata/1/pubpaa/US10_RUB_PUB.pep:*
gnz_6/ptodata/1/pubpaa/US60_RUB_PUB.pep:*
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6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
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US-10-307-724-2

US-10-006-593-35

US-10-006-593-37

US-10-006-593-39

US-10-006-593-43

US-10-006-593-43

US-10-006-593-45

US-10-006-593-49

US-10-006-593-49

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US-10-006-593-49
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Sequence 2, Appli
Sequence 3, Appli
Sequence 35, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 39, Appli
Sequence 41, Appli
Sequence 43, Appli
Sequence 45, Appli
Sequence 49, Appli
Sequence 64, Appli
Sequence 31, Appli
Sequence 31, Appli
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ALIGNMENTS	US-10-307-724-37 US-10-307-724-39 US-10-307-724-43 US-10-307-724-45 US-10-307-724-45 US-10-307-724-66 US-10-307-724-130 US-10-307-724-130 US-10-307-724-125 US-10-307-724-124 US-10-307-724-124 US-10-307-724-124 US-10-307-724-16-31 US-10-603-768-13 US-10-609-7217-26 US-10-609-7217-26 US-10-609-7217-26 US-10-609-7217-26 US-10-609-7217-29 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-609-7217-30 US-10-632-388-32 US-10-651-723-33
	Sequence 37, Appl Sequence 41, Appl Sequence 43, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 125, Appl Sequence 126, Appl Sequence 127, Appl Sequence 127, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 193, Appl Sequence 13, Appl Sequence 13, Appl Sequence 26, Appli Sequence 13, Appl Sequence 13, Appl Sequence 27, Appli Sequence 28, Appl Sequence 29, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 24, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 21, Appl Seque

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; OTHER INFORMATION: TPO mimetic with flanking amino US-10-006-593-2
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                                                                       Query Match
Best Local S
Matches 15
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Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                  ORGANISM: artificial sequence
                                                                         15;
                                    1 IEGPTLROWLAARAP 15
                                                                                        Similarity
IEGPTLROWLAARAP 15
                                                                         Conservative
                                                                                        100.0%;
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                                                                     Score 80; DB
Pred. No. 1.3
0; Mismatches
                                                                         1.3e-05;
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INFORMATION:

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; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-31
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; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-2
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PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
                                         Matches
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                       SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/10006593 Publication No. US20030049683A1 GENERAL INFORMATION:
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SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Frederickson, Shana
APPLICANT: Renbhaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana
                                                                                                                                                                         TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2002-12-02
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TLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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IEGPTLRQWLAARAP 15
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                                       Conservative
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                                                    100.0%; Score 80; DB 14; Length 18; 100.0%; Pred. No. 1.6e-05;
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Pred. No. 1.3e-05;
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT ETLING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR PRICING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 37
LENGTH: 18
                                                                                                    ; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-37
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PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 35
LENGTH: 18
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Best Local Similarity
Matches 15; Conserva
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Query Match 100.0%; Score 80; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
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APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
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ORGANISM: artificial sequence
FEATURE:
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                                         DB 14; Length 18;
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Query Match
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Tatches 15; Conserve
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; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-39
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
                                                                                      ; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-41
                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
LENGTH: 18
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Query Match 100.0%; Score 80; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana
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APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
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                                                                                                                              ORGANISM: artificial sequence FEATURE:
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Pred. No.
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                                        Length 18;
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; TYPE: PRT; ORGANISM: artificial sequence; PEATURE: FEATURE: OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-43
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                                                         ; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-006-593-45
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
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US-10-006-593-45
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 43
LENGTH: 18
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Query Match
Best Local Similarity
                                                                                                                                                                                SEQ ID NO 45
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APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
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PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
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SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
                                                                                               LENGTH: 18
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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100.0%;
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Score 80;
Pred. No.
DB 14; Length 18
1.6e-05;
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; OTHER INFORMATION: TPO mimetic peptide with flanking sequence US-10-006-593-66
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CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR PPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
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         Query Match
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NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version
SEQ ID NO 66
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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                                                                        TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bowdish, Katherine S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
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                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               uence 66, Application US/10006593
Lication No. US20030049683A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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Similarity 100.0%;
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                                                                                                                                                              version 3.1
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     100.0%;
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 Score 80;
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Pred. No. 1.6e-0
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DB 14; Length 18;
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APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT ETLING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR APPLICATION DOS: 1134
                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR APPLICATION NUMBER: US 10/006,593
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US-10-307-724-35
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US-10-307-724-31
                                                                    NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn versic
SEQ ID NO 35
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SEQ ID NO 31
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Best Local Similarity
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Matches 1
                                                                                                                                   PRIOR FILING DATE: 2001-12-05
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2019
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bowdish,
APPLICANT: Frederic
APPLICANT: Renshaw
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
FEATURE:
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APPLICANT: Bowdish, Katherine S.
APPLICANT: Erederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-05-09
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US-10-307-724-39
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; OTHER INFORMATION: TPO mimetic with flanking amino acids US-10-307-724-37
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2clp
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-05
PRIOR FILING DATE: 2001-05-07
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PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn version 3.2
SEQ ID NO 37
LENGTH: 18
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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Publication No. US20030232972A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: artificial sequence
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Local Similarity 100.0%; Pred. No. 1.6e-05;
hes 15; Conservative 0; Mismatches 0;
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Pred. No. 1.6e-05;
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SEQ ID NO 39
LENGTH: .18
TYPE: PRT
                                                      Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                            ORGANISM: artificial sequence FEATURE:
                                                                                                                              OTHER INFORMATION: TPO mimetic with flanking amino acids
                        1 IEGPTLROWLAARAP 15
                                                       Conservative
                                                                   100.0%; Score 80; DB 14; 100.0%; Pred. No. 1.6e-05;
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                                                         Mismatches
                                                                                Length 18;
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Search completed: December 20, 2004, 14:06:44 Job time : 144 secs

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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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1: pir1:*
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Match Length
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Gapop 10.0 , Gapext 0.5
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membrane protein,
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probable phosphopa
hypothetical 21.8K
ABC transporter, A
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glyceraldehyde-3-p
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probable dimethyla
protein kinase [im
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probable membrane
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RESULT 2 AGG147 probable membrane prote: C;Species: Yersinia pess C;Date: 02-Nov-2001 #sec C;Accession: AG0147 R;Parkhill, J; Wren, B deno-Tarraga, A.M.; Chi: il, M.; Rutherford, K.; Nature 413, S23-527, 200 A;Title: Genome sequence, A;Reference number: AB0 A;Accession: AG0147 A;Status: preliminary	Oy 2	Query Matc Best Local Matches	A; Gene: cbt A; Start coc C; Superfam: C; Keywords:	A; Molecule A; Residues A; Cross-ref	A,Reference number: \$13573; MUID:91172133; PMA;Accession: \$13578	A; Title: Ch A; Reference A; Accession A; Status: I	C;Date: 04- C;Accession C;Accession R;van den E	RESULT 1 A36925 transcripti		& & & & & & & & & & & & & & & & & & &	
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prane protein YPO1203 [presinia pestis v-2011 #sequence_revis AG0147 J; Wren, B.W.; Thomson A.M.; Chillingworth, priord, K.; Simmonds, M 323-527, 2001 ms sequence of Yersini number: AB0001; MUID:21 AG0147 AG0147	ig-ptlrowlaara : iglpvvrowlavra	nilarity Conserva	TG ranscrip binding;	DNA 0 <mei></mei>	es: UNIF Arnberg, Arzs, 32 225, 32 ication per: S135	LyeR-ty ber: A369 1925 ninary	994 #seq 925; S13 E.R.E.;	tivator		5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
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impos ion (, N.I T.; (T.; S) .; S)	ω	Score Pred. 2; Mis	ivator I	,	45; EMBI nequist, 991 nization :9117213	cription :9401246	vision (408 zen, L.;	e CbbR -	ALIG	AE2719 \$25204 C70653 \$27491 AD2315 AB1958 E81015 H69878 \$30484	A35080 DEIS3C JQ1287 B70936 G87552 B95325 A97501
- Yersinia p v-2001 #text_ itball, R.W.; n, A.; Davies n, J.; Steven the causativ MID:11586360		DB 2; L. .5; es 2;	LysR-type regulation		05; NID:g297; Terpstra, arbon dioxid ID:1900916	tivator, is ID:8407781	-1994 #text er, W.G.	- Xanthobacter flavus	ALIGNMENTS	And the second	
pestis (strain CO92) change 09-Jul-2004 ; Holden, M.T.G.; Prentice, M.B! ss, R.M.; Davis, P.; Dougan, G.; ns, K.; Whitehead, S.; Barrell, ve agent of plague.		ength 333; Indels 1; Gaps 1;			851; PIDN:CAA80406.1; PID:g581 P.; Lidstrom, M.E.; Dijkhuizen e fixation genes in Xanthobact	required for expression of the	_change 09-Ju1-2004	พนธ		topoisomerase IV s smmX protein - Str probable prephenat hypothetical prote hypothetical prote probable permease ABC transporter, p probable protein k pol polyprotein -	glyceraldehyde-3-p glyceraldehyde-3-p glyceraldehyde-3-p probable serine/th conserved hypothet conserved hypothet topoisomerase iv c

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A;Molecule type: DNA
A;Residues: 1-296 «KUR»
A;Crose-references: UNIP)
C;GenetLcs:
A;Gene: YPO1203
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A; Residues: 1-400 <S
                                                                                                                                                                                                         A; Accession: C87021
A; Status: preliminary
                                                                                                                                                                                                                                         Nature 409, 1007-1011, 2001

A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A; Title: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                serine-threonine protein kinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: C87021 R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; eam, M.A.; Rutherford, K.M.
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandresm, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: galU
C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
C;Keywords: nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galU [similarity] C;Species: Mycobacterium tuberculosis C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                    Superfamily: Mycobacterium tuberculosis probable
                                                                                                                Gene: ML0897
                                                                                                                                           Cross-references: UNIPROT:069568; GB:AL450380; NID:gl3092968;
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                                57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%;
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Pred. No. 5.3;
1; Mismatches
                                  Score 46;
Pred. No.
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Pred. No.
            Mismatches
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              4
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                                                            RESULT 7
probable glutathione transferase (EC 2.5.1.18)
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1
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A;Map position: 4
A;Introns: 45/1; 76/1; 111/3
C;Superfamily: glutathione transferase
                                                                                                                                                                                                A; Gene: CESP: K08F4.11
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A; Experimental source: clone K081
                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-200 <WIL>
                                                                                                                                                                                                                                                                                                                      R;Hembry, C. submitted to the EMBL Data Library, A;Reference number: Z19746
A;Accession: T23485
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein K08F4.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T23485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gene: GTG
F;388-415/Domain: DNA binding #status predicted <DNA>
F;405-415/Region: helix-turn-helix
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A;Residues: 1-436 <COR>
A;Residues: 1-436 <COR>
A;Cross-references: UNIPROT:Q45293; EMBL:Z66534
A;Experimental source: ATCC 13869
A;Note: The authors translated the initiation codon TGT for residue
A;Note: The authors translated the codon ATT for residue 125 as Tyr
A;Note: the source is designated as Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 170, 91-94, 1996
A;Title: Cloning and characterization of an IS-like element
A;Reference number: JC4742; MUID:96200862; PMID:8621097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transposase - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change
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JC4742
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                                                                       Matches
                                                                                                          Query Match
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                                                                   Conservative
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                                                                                                                                                                                                                                     clone K08F4
                                                                                    55.0%;
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                                                                                                                                                                                                                                                   PIDN:CAA93088.1; GSPDB:GN00022; CESP:K08F4.11
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                                                                                  Score 44; I
Pred. No. 7
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                                                                   Mismatches
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7.3;
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03-Dec-1999

#text_change 09-Jul-2004

GST3 -

Caenorhabditis elegans

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A;Molecule type: DNA
A;Residues: 393-536 (LIU)
A;Residues: 393-536 (LIU)
A;Crouse-references: GB.M24148; NID:g304949; PIDN:AAA16101.1; PID:g450380
C;Comment: The enzymatic steps in the condensation of L-serine and 2,3-dihydroxybenzoic ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with ty is based on its recognized homology with the coumarate-CoA ligase and by analogy with the coumarate-CoA ligase and by a
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A; Residues: 1-368, ECRRKSTAAR', 379-536 <STA>
A; Residues: 1-368, ECRRKSTAAR', 379-536 <STA>
A; Cross-references: GB:M27490; EMBL:X15058; NID:g41345; E
R; Liu, J; Duncan, K.; Walsh, C.T.
J. Bacteriol. 171, 791-798, 1989
A; Title: Nucleotide sequence of a cluster of Escherichia
A; Reference number: A91904; MUID:89123155; PMID:2521622
A; Accession: A32047
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A;Molecule type: DNA
A;Residues: 1-536 <BLAT>
A;Residues: 1-536 <BLAT>
A;Cross-references: UNIPROT:P10378; GB:AE000165; GB:U00096; NID:g1786808;
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
R;Staab, J.F.; Elkins, M.F.; Earhart, C.F.
FEMS Microbiol. Lett. 59, 15-19, 199
FEMS Microbiol. Lett. 59, 15-19, 199
A;Title: Nucleotide sequence of the Escherichia coli entE gene.
A;Reference number: A48308; MUID:89290355; PMID:2525505
A;Note: in MedLine 89290355 this citation is erroneously given as volume 5
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A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: H64792
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                                          A,Pathway: enterobactin biosynthesis
A,Note: this is one component of a membrane-bound multienzyme complex that catalyzes the
for transport into the cell
                                                                                                                                                                                                                               A; Map position:
C; Function:
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                                                                                                                                                                               A, Description: catalyzes the formation
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;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,3-dihydroxybenzoate-[carrier protein] ligase (EC 6.2.1.-) entE -,Alternate names; 2,3-dihydroxybenzoate-AMP ligase [misnomer]; dil
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;Tawe, W.N.; Eschb
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4-coumarate-CoA ligase;
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Pred. No. 7.6;
2; Mismatches
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acetate-CoA ligase homology
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A;Reference number: A85480;
A;Accession: E85558
A;Statue.
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F; 69-526/Domain:
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                                                                                                                                                                                                                   DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99708
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2,3-dihydroxybenzoate-AMP ligase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A99708
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                                                                                                               C;Superfamily:
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                                                                                                                                                                                                                                                                                                         R; Hayashi, T.;
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C;Superfamily:
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R;Perna, N.T.; Plunl
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                                                                                                                                                                                                                                                                                         gasawara, N.; Yasunaga,
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                                                                                                                                                                                        A;Residues: 1-536 <HAY>
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Yasunaga, T.; Kuhara,
                                                                                                               4-coumarate-CoA ligase; acetate-CoA
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57.1%;
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MUID:21074935; PMID:11206551
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                                                                      Score 44;
Pred. No.
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Pred. No. 20;
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Shiba, T.; Hattori,
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A.; Dimalanta,
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n EDL933
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                                                                                                                                                           PIDN:BAB34056.1;
RIMD 0509952
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anta, E.;
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Potamousis,
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K.; Apodaca
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RESULT 11

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C;Accession: H83415
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Olson, M.V.
.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cis/trans isomerase PA1846 [imported] - Pseudomonas aeruginosa (C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change C;Accession: H83415
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H83415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
               A; Molecule type: DNA
A; Residues: 1-204 < MIR>
A; Cross-references: UNIPROT: 034294;
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C;Species: Bacillus halodurans
 A; Cross-refere
A; Experimental
                                                                                                                                                                                                                       thiamine-phosphate diphosphorylase
                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83415
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A;Residues: 1-762 <STO>
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A,Experimental source: strain C-125
                                                               Miranda-Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, Bacteriol. 179, 6887-6893, 1997
Fittle: Expression of thiamin biosynthetic genes (thiCOGE) and product Reference number: Z22737; MUID:98037482; PMID:9371431
RACCESSION: T44257
RACCESSION: T44257
                                                                                                                                                                     Species: Rhizobium etli
;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
;Accession: T44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Cross-references: UNIPROT:Q912P9; GB:AE004610; GB:AE004091; NID:g9947825; PIDN:AAG0523
;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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   source: strain
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46.7%;
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Pred. No.
                                                                                                                                                                                                                       (EC 2.5.1.3) [imported] - Rhizobium etli
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                   EMBL: AF004408; NID: g2627325; PIDN: AAC45975.1;
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K.; Lim,
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                   PID:g2
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A; Residues: 1-285 < COL>
A; Cross-references: UNI
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                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-664 < KUR>
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A; Title: Complete genome 8
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                                                    Matches
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                                                                                                                                                  Experimental
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Best Local &
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8, Conserv
IEGPTLRQWLAARAP
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                                                                    53.8%;
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C;Accession: G89894

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: G89894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid b
C;Superfamily: thiE protein; thiamin-phosphate
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable dimethyladenosine transferase (ksgA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                   A; Cross-references: UNIPROT: Q99UP8; A; Experimental source: strain N315
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se: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of Treponema pallidum,
so; MUID:98332770; PMID:9665876
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Pred. No.
4.
                     Score 43;
Pred. No.
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L; Mismatches
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  Mismatches
                     36;
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02-MAR-2004
Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapu
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017230, AA503241 L; -
SEQUENCE 302 AA; 32149 MW; 4E5D2B1AB572BAE7 CRC64;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AE017230; AASO3241.1; -.
InterPro; IPR005835; NTP_transferase.
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Bacteria; Actinobacteridae; Actinom
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STRAIN=k10;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296
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81.8%;
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Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4E5D2B1AB572BAE7 CRC64;
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 Query Match
Best Local S
Matches 10
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Best Local S
Matches 9
                                                                  Pfam; pF00126; HTH 1; 1.

Pfam; pF03466; LysR substrate; 1.

PFRINTS; PR00039; HTHLYSR.

PROSTITE; PS50931; HTH LYSR; 1.

PROSTITE; PS50931; HTH LYSR; 1.

ACTIVATOR; DNA-binding; Transcription regulation.

ACTIVATOR; DNA-binding; Transcription regulation.
                                                      DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    EMBL; Z22705; CAA80406.1;
EMBL; X17252; -; NOT_ANNOT
PIR; A36925; A36925.
                                                                                                                                                         InterPro; IPR000847; HTH_LygR.
InterPro; IPR005119; LygR_subst.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                               "Identification and organization of carbon dioxide fixation genes Xanthobacter flavus H4-14.";
Mol. Gen. Genet. 225:320-330(1991).
-!- FUNCTION: Transcriptional activator for the cbb operon (cbbLS for RuBisCO and other Calvin cycle genes. Binds specifically two binding sites in the cbbR-cbbL intergenic region.
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLINE=94012468; PubMed=8407781; van den Bergh E., Dikhnizen L., Meijer W.G.; "CbbR, a LygR-type transcriptional activator, is reexpression of the autotrophic CO2 fixation enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91172133; PubMed=1900916;
Meifer W.G., Arnberg A.C., Enequist H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyphomicrobiaceae, Xanthobacter
NCBI_TaxID=281,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
05-UL-2004 (Rel. 44, Last annotation update)
HTH-type transcriptional regulator cbbR (RuBisCO transcriptional regulator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel.
01-OCT-1996 (Rel.
05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XANFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-150 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=cbbR; Synonyms=cfxO;
Xanthobacter flavus
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  l Similarity
10; Conserv
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9; Conserv
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                                                 333
  Conservative
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                                                      41 F
36003 MW;
            61.9%;
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Score 49.5; D
Pred. No. 7.2;
2; Mismatches
                                       HTH lysr-type.
H-T-H motif (By similarity).
, 9B375B4FB2D1EE73 CRC64;
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Pred. No. 5.4;
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••
                        1; Length 333;
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zymes of Xanthobacter
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RESULT 5
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AC QPRX
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DT 01-
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Best Local
                                                                                                    STRAIN=3(2) / M145;

STRAIN=3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins I

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., O'Neil

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill
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Q8Y015;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                           Hopwood D.A.;
"Complete genome sequence coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9RKM5 PRELIMINARY; PRT; 319 AA. Q9RKM5; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2004 (TrEMBLrel. 26, Last annotation update) Putative MerR family transcriptional regulator. OrderedLocusNames=SCO4102; ORFNames=SCD17.06c;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FRO
STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Génin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum.", Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
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Complete proteome; Hypothetical protein.
SEQUENCE 91 AA; 10321 MW; 2B4DFFEB37A528AD CRC64;
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Name=RS04149, OrderedLocusNames=RSc1059;
Ralstonia solanacearum (Pseudomonas solan Bacteria; Proteobacteria; Betaproteobacte Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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   417:141-147 (2002)
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46.7%;
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Last annotation updat
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                                                                 the model
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Pred. No. 2
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                                                                                                                                                                                                                          Colling M., Howarth S., O'Neil S.,
                                                                                                                                                               Taylor K.,
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Best Local &
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Best Local
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                                                                                                                                                                                                                            GO; GO:005515; F:protein binding; IE
InterPro; IPR000210; BTB POZ.
InterPro; IPR000210; BTB POZ.
InterPro; IPR002083; MATH.
Pfam; PF00051; BTB; 1.
Pfam; PF00917; MATH; 1.
SMART; SM00225; BTB; 1.
SMART; SM00061; MATH; 1.
SMART; SM00061; MATH; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50144; MATH; 1.
SEQUENCE 375 AA; 41043 MW; 20FC6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TremBLrel. 25, Created)
01-MAR-2004 (TremBLrel. 26, Last sequence update)
05-UTL-2004 (TremBLrel. 27, Last sequence update)
05-UTL-2004 (TremBLrel. 27, Last annotation update)
0SUNBA0053K19.27 protein (OSUNBb0060B0.2 protein).
Name=OSUNBA0053K19.27; Synonyms=OSUNBb0060E08.2;
OYYZA sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae, Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL939118; CAB56383.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; Firenaceription factor activity; IEA.
GO; GO:00003700; Firenaceription of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000051; HTH_MerR.
InterPro; IPR000051; Putativ_DNA_bind.
Pfam; PF00376; MerR; 1.
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Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
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SMART; SM00422; HTH MERR; 1.

PROSITE; PS50937; HTH MERR 2; 1.

Complete proteome; DNA-binding.

SEQUENCE 319 AA; 34841 MW; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL606645; CAE03519.2; -.
EMBL; AL606669; CAE04739.1; -.
Gramene; Q7XPP6; -
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Han B.;
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138
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                                                          IEGPTLRQWLAARAP 15
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                                                                                                              ; Score 49; DB; Pred. No. 9.9; 1; Mismatches
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Pred. No. 8.4;
2; Mismatches
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Q918BA
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DT 01-0
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COC SOTA
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09L8D4;
01-OCT-2000
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sanotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
Name=RS02135; OrderedLocusNames=RSp1579;
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Molnar I., Schupp T., Ono M., Zikkle R.E., Milnamow M.,
Nowak-Thompson B., Engel N., Toujekle R.E., Stratmann A., Cyr D.D.,
Gorlach J., Mayo J.M., Hu A., Goff S., Schmid J., Ligon J.M.;
"The biosynthetic gene cluster for the microtubule-stabilizing epothilones A and B from Sorangium cellulosum So ce90.";
Chem. Biol. 7:97-109 (2000).
EMBL, AP210843; AAF26904.1; -.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
12-OCT-2003 (TrEMBLrel. 25, Last annotation update)
13-OCT-2003 (TrEMBLrel. 25, Last annotation update)
14-OCT-2004 (TrEMBLrel. 15, Created)
15-OCT-2004 (TrEMBLrel. 15, Created)
16-OCT-2004 (TrEMBLrel. 15, Last sequence update)
16-OCT-2004 (TrEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Plasmid megaplasmid.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
GO; GO:000562; C:intracellular; IEA.
GO; GO:000570; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009059; bi_resp_regltr_C.
InterPro; IPR002197; HTH_Fis.
InterPro; IPR002197; HTH_LuxR.
Pfam; PF00196; GerE; 1.
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NON TER 1
SEQUENCE 607 AA; 6
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Pred. No. 19;
3; Mismatches
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Best Loc
Matches
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                      He J.G., De Chan S.M.;
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Q9WWZ0;
01-NOV-1999
01-NOV-1999
01-MAR-2004
                                                                     SEQUENCE FROM N.A.
MEDLINE=21874810; PubMed=11878882;
He J.G., Deng M., Weng S.P., Li Z.,
                                                                                                                                                                                           Infectious spleen and kidney Viruses; dsDNA viruses, no RN unclassified Iridoviridae. NCBI_TaxID=180170;
   "Complete genome
kidney necrosis
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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PRINTS; PR00038; HTHLUXR.
PRODOM; PD000307; HTH LUXR; 1.
SMART; SM00421; HTH LUXR; 1.
Complete proteome; DNA-binding;
SEQUENCE 252 AA; 27666 MW; 4
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InterPro; IPR010706; CTI.
InterPro; IPR010345; CytC_heme_BS.
InterPro; IPR009056; Cytochrome_c.
Pfam; PF06934; CTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Involvement of the cis/trans isomerase Pseudomonas putida DOT-TIE.";
J. Bacteriol. 181:5693-5700(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Junker F., Ramos J.L.; "Involvement of the ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99412268; PubMed=10482510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=cti;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00190; CYTOCHROME C; UNKNOWN 1
766 AA; 87058 MW; A4A0FC6C22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGPTLRQWLAARAP
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                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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   e analysis of the mandarin 
iridovirus.";
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21,
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26,
                                                                                                                                                                                                                                                              RNA
                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
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Pred. No. 9.8;
3; Mismatches
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                                                                           Long Q.X.,
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                                                                           Wang X.Z.,
                     apleen
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Best Local S
Matches 7
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SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
STRAINB=2137863; PubMed=12142430;
MEDLINB=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
                                                                                                                                                                                                                                                                                                                           PIR; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang R.;
Submitted (APR-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CO-92 / Biovar Orientalis;

MEDLINS=21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyehev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.",

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8ZGS7 PRELIMINARY; PRT; 296 AA. Q8ZGS7, Q74WE0; Q7CH89; Q1-MAR-2002 (TYEMBLYE1. 20, Created) Q1-MAR-2002 (TYEMBLYE1. 20, Last sequence update) Q1-OCT-2004 (TYEMBLYE1. 28, Last annotation update) Putative membrane protein (Putative transmembrane protein (Putative transmembrane protein (Putative transmembrane protein) Putative transmembrane protein (Putative transmembrane protein 
                                                                                                                                                                                                                        Pfam; PF00892; DUF6;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ414147; CAC90042.1;
EMBL; AE013900; AAM86536.1;
EMBL; AE017130; AAS61189.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y.,
Han Y., Pang X., Zhai J., Chen F.,
Ye C., Du Z., Lin W., Wang J., Yu J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol.
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EMBL; AF371960; AAL98838.1;
SEQUENCE 941 AA; 106703
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Yersinia pestis
J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae;
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                                                                                                                                                                                                                                                                               ; AG0147; AG0147.
GO:0016021; C:integral to
GO:0016020; C:membrane; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581 VQGPTLAQWICSTA 594
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7; Conserv
       Similarity 81.
9; Conservative
                                                                                                                                           proteome;
296 AA;
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                                                                                                                                                                                                                                                         IPR000620; DUF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                  Transmembrane.
                                    58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₩.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
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Pred. No. 36;
4; Mismatches
                                        Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                               membrane; IEA
                                                                                                                                               45947413DCD54CFF CRC64;
Mismatches
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                                 No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang J., Pei
Qin H., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIM. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
36;
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ang J., Li S., Gu
., Wang J., Huang
                                                                     Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang
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                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Q888B5 PRELIMINARY;
Q888B5;
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Creat
01-JUN-2003 (TrEMBLrel. 24, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Similar to RIKEN CDNA 2010110K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80ZR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases EMBL; AE017130; AAS61189.1; - SEQUENCE 296 AA; 31378 MW; 45947413DCD54CFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-91001 / Blovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D.,
Song Y., Tong Z., Zhai J., Chen F., Qin H., Wang J., I
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang Yang R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2004 (TrEMBLrel.
24-MAR-2004 (TrEMBLrel.
04-MAY-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative membrane RHAT4 OR YP0934.
                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS61189
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                               NON TER
                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             BC048547; AAH48547.1;
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8; Conserv
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llarity 81.8%;
Conservative
                                     PRELIMINARY;
                                                                                                                                                                                         Conservative
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61.5%;
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                                                                                                                                                                                       Score 46; DB
Pred. No. 13;
1; Mismatches
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Sciurognathi;
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annotation update)
gene (Fragment).
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annotation update)
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                                                                                                                                                                                                                         Length 153;
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; Murinae; Mus
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Li S., Guo
J., Huang
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Best Local S
Matches
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
-!-SIMILARITY: Contains 1 HTH luxR-type DNA-binding domain.
EMBL; AL646067; CAD15597.1; -.
HSSP; P11470; IFSE.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005700; F:transcription factor activity; IEA.
GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
InterPro; IPR000959; bi resp. regltr_C.
InterPro; IPR000792; HTH_LuxR.
                                                                                                                                                                     MEDLINE=21661879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Salanoubat M., Genin S., Artiguenave F., Caus J.C., Cattolico L., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane protein, putative.
OrderedLocusNames=PSPTO1115;
                                                                                                                                                                                                                                                                                               STRAIN=GMI1000
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Burkholderiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 167 AA;
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9; Conservative
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OBXY68 PRELIMINARY; PRT; 252 AA.

OBXY68; O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)

PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.

Name=RS03457; OrderedLocusNames=RSC1895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Wartin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A.; "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000."; Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001220; Lectin_legB.
PROSITE; PS00307; LECTIN_LEGUME_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100; Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonadaceae; Pseudomonas.
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Pred. No. 1
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DNA-dependent; IEA.

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DR Pfam; PF00196; GerE; 1.

DR PRINTS; PR000307; HTHLUAR; 1.

DR SMART; SM00421; HTH_LUXR; 1.

KW Complete proteome; DNA-binding; Transcription regulation.

SQ SEQUENCE 252 AA; 27945 MW; 17FD89DC6803EFBF CRC64;

Query Match
Best Local Similarity 46.7%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEGPTLROWLARRAP 15
Db 76 IDTPLMRRWFATRSP 90

Search completed: December 20, 2004, 13:54:17

Job time: 192 secs
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